REMARKS

After entry of this amendment, claims 1, 3-18, and 20-25 are pending, of which claims 4-6, 16-18, and 20-21 are withdrawn. The claims have been amended without prejudice or disclaimer to delete the non-elected subject matter, to correct typographic error, to better comply with the U.S. practice, and to address various points made in the Office Action. The amended claims find support *inter alia* in the original claims. Claim 1 finds further support in the specification at page 5, lines 9-11, page 22, lines 18-22, page 25, line 42, page 34, lines 2-13, and page 35, line 28. Claim 7 finds further support at pages 54-56, Examples 6-7. Claims 15 and 24 find further support at page 46, lines 20-32. No new matter has been added.

Withdrawn method claim 16 has also been amended without prejudice or disclaimer to require all the limitations of the product claims. Support is found *inter alia* in the original claims. Further support is found in the specification at page 5, lines 9-11, page 22, lines 18-22, page 25, line 42, page 34, lines 2-13, and page 35, line 28. No new matter has been added. In the event that the product claim is found allowable, rejoinder of the withdrawn method claims is respectfully requested. MPEP § 821.04(b).

In the specification, pages 7 and 59-61 have been amended to insert the sequence identifier numbers as required by the Examiner. Furthermore, trademarks appeared at pages 51-53 and 56 have been capitalized and a generic terminology has also been provided. No new matter has been added.

Specification

Sequence Identifier Number

The Examiner requires that the sequences recited in Figures 6, 7, and 8 and in the Tables at page 60-61 be identified by sequence identifying numbers and be included in the Sequence Listing. In response, Applicants submit herewith a replacement copy of the Sequence Listing that conform to 37 CFR §§ 1.821-1.825 in electronic format as text file *via* EFS-Web accompanied by a Statement to Support Filing and Submission in Accordance with 37 CFR §§ 1.821-1.825. The corresponding sequence identifiers have also been added to the brief description of Figures 6, 7, and 8 at page 7, and in the Tables at pages 59-61 of the specification to comply with 37 CFR § 1.821(a) and (d). The specification has also been amended adding the

required paragraph to incorporate by reference the text file of the Sequence Listing submitted *via* EFS-Web as per 37 CFR § 1.52(e)(5). No new matter has been added to the Sequence Listing. Entry of this Sequence Listing into the application is requested.

Trademark Use

The Examiner requires that the trademarks appeared in the specification be capitalized or denoted with the registered trademark symbol, and be accompanied by the generic terminology. In view of the amendment, withdrawal of this objection is respectfully requested.

Information Disclosure Statement

A Supplemental Information Disclosure Statement is filed hereinwith. Applicants respectfully request that the Examiner consider and make of record the references cited in the Supplemental Information Disclosure Statement.

Claim Objections

The Examiner objects to claims 1, 7, and 9 for informalities. Claims 1, 7, and 9 have been amended without prejudice or disclaimer by adopting the Examiner's suggestions made in the Office Action. In light of the amendment, reconsideration and withdrawal of the objections are respectfully requested.

Claim Rejections – 35 USC § 112, Second Paragraph

The Examiner rejects claims 1, 3, 7-9, 11-15 and 22-25 as being indefinite for reciting relative terms "predominant," and "essentially." The Examiner further finds claim 1 indefinite for the recitation of "100 base pair nucleic acid" in subpart i) of part c). Applicants respectfully disagree. However, to expedite prosecution, the claims have been amended without prejudice or disclaimer to delete the aforementioned recitations. It is believed that the present amendment renders the rejections moot.

Claims 1, 3, 7-9, 11-15 and 22-25 are further rejected as being indefinite for reciting "substantially." Applicants respectfully disagree.

"The fact that claim language, including terms of degree, may not be precise, does not automatically render the claim indefinite. . . . Acceptability of the claim language depends on whether one of ordinary skill in the art would understand what is claimed, in light of the

specification." MPEP § 2173.05(b). Thus, the term "substantially" is definite where the general guidelines were provided in the specification or when one of ordinary skill in the art would know what was meant by that term. See MPEP § 2173.05(b), subsection D.

Here, the term "substantially" recited in the claims is definite in view of the general guidelines provided in the specification. For instance, the specification at page 23, lines 15-28, defines what the term "substantially all vegetative plant tissues or organs" means. The specification further provides the general guidelines as to the meaning of this term at page 19, lines 12-25, by referring to the Example and Figures in the specification. Thus, one of ordinary skill in the art, when reading the specification, would understand what this term means. Accordingly, it is respectfully submitted that the term "substantially" as used in the claims is definite. Reconsideration and withdrawal of the rejection is respectfully requested.

Claim 7 is further rejected as being indefinite for omitting essential elements. In response, claim 7 has been amended without prejudice or disclaimer to specify that the nucleic acid of interest encodes an enzyme having glucoronidase activity. Reconsideration and withdrawal of this rejection is respectfully requested.

Claim Rejections – 35 USC § 112, First Paragraph

The Examiner rejects claims 1, 7-15 and 22-25 for allegedly failing to comply with the written description requirement and for lack of an enabling disclosure. Applicants respectfully disagree. However, to expedite prosecution, the claims have been amended without prejudice or disclaimer to recite the components of the claimed expression cassette with more specificity. Applicants respectfully request reconsideration in light of the amendment and for the following reasons.

Written Description Rejection

The Examiner alleges that the specification describes only the promoter of SEQ ID NO: 1 or its complement, but not equivalents or variants of SEQ ID NO: 1. The Examiner further asserts that the specification fails to describe a representative number of species from within the claimed genus, and, fails to disclose what structural features are common to members of the claimed genus. Applicants respectfully disagree and submit that the claims as amended encompass only subject matter which is clearly described.

"A description of a genus of cDNAs may be achieved by means of ... a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus." *The Regents of The University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). As the Examiner acknowledged, the specification describes motifs identified in the nucleotide sequence of SEQ ID NO: 1. Office Action at page 9. Additionally, the specification further describes, in an indirect manner, the motifs or regions of SEQ ID NO: 1 that are unique and most likely related to the promoter function.

As described in the specification at page 18, lines 21-41, the ptxA gene shares a significant homology with numerous genes at both the nucleotide and the polypeptide level. However, the ptxA promoter of the present application possesses a tissue-specific, stress-independent expression profile that is very different from the expression patterns of some other promoters that have a significant sequence homology as compared with the ptxA promoter. For example, as shown in Figure 7 and further described in the specification at page 18, the promoter region of the ptxA gene (the "ptxA promoter") has approximately 50%, or as high as 87% over 100 consecutive base pairs, sequence identity to the promoter region of *Medicago sativa* proline-rich protein (MsPRP2) gene (the "MsPRP2 promoter"). However, the MsPRP2 promoter has been shown to be root-specific and salt-inducible, which is significantly different to the expression pattern of the ptxA promoter (*i.e.* in substantially all vegetative plant tissues). Thus, one skilled in the art would be guided by an initial presumption that the sequences identical between the MsPRP2 promoter and the ptxA promoter are likely **not** responsible for the specific expression pattern of each individual promoter. Conversely, the sequence that is unique to the ptxA promoter is more likely correlated to the promoter function and the tissue specificity. Together with the table of Example 14 at page 60, one ordinary skill in the art would be able to identify which regions or motifs would likely be important for the promoter function and the tissue specificity of the ptxA promoter, and should not be deleted or modified. Examples of such regions or motifs are the AMYBOX2, C8GCARGAT, CAATBOX1, IBOXCORENT, POLASIGl, POLASIG2 and POLASIG3 sequence elements. Accordingly, it is respectfully submitted that the specification provides disclosure of structure which provides an adequate description to convey possession of the genus of the promoter sequences as recited in the amended claims.

In light of the amendment, Applicants respectfully submit that the claims satisfy the written description requirement. Reconsideration and withdrawal of the rejection is respectfully requested.

Enablement Rejection

The Examiner alleges that the specification is enabling only for SEQ ID NO: 1, but not equivalents or variants thereof. The Examiner further argues that the art is so unpredictable as to make any homologs or variants that retain promoter activity of SEQ ID NO: 1 non-enabled, citing various references. Additionally, the Examiner notes that the promoter causes different expression patterns in different plants. Applicants respectfully disagree that the claims as amended are not enabled.

The Examiner alleges that the specification does not provide guidance for any sequence variants of SEQ ID NO: 1. The Examiner argues that mutation of promoter sequences produces unpredictable results, citing Donald *et al.* (hereinafter "Donald"). The Examiner further alleges that the region of a given promoter with a specific activity cannot be predicted and involves complex interaction of different subdomains, citing Benfey *et al.* (hereinafter "Benfey"). Additionally, the Examiner cites Kim *et al.* (hereinafter "Kim") to support the position that even a small region may be critical for activity and such criticality must be determined empirically. Applicants respectfully disagree with the Examiner's characterization of these references.

Donald defined a 196-bp long fragment of the *Arabidopsis thaliana* rbc8-1A promoter as being essential and sufficient for promoter activity (page 1717, Abstract). Donald showed that this promoter fragment had the capacity to direct expression independent of its orientation and relative position in the *Adh* promoter. Further sequence analysis showed that this promoter fragment contained further promoter elements necessary for its activity (page 1717, Abstract and page 1720, Figure 3). Donald also disclosed that the expression pattern of the promoter fragment can be influenced by other active promoter fragments and enhancing elements contained in the CaMV promoter fragment and the *Adh* promoter used by Donald (page 1724, last paragraph). This does not show that mutation of promoter sequence produces unpredictable results. Rather Donald showed that active fragments and elements from other promoters could restore activity following mutations in essential boxes (see Abstract and page 1724). Donald also demonstrated that a promoter fragment identified by deletion analysis can be used independent of its

orientation and relative position and still preserve its activity, as long as particular sequence elements like the G-, I- or GT-box are not destroyed by mutation (page 1724, last paragraph). Those boxes have a size of only 12 to 14 base pairs (page 1720, Figure 3) and represent only a minor part of the rbcS-1A LRE sequence of 196 base pairs. Moreover, the mutations described in Donald were site-specific mutations in conserved sequences and not random mutations (see Abstract).

Similarly, Kim actually supports enablement. Kim discloses a mutational analysis of an essential part of 30 nucleotides of the *nos* promoter (pages 106 and 107, first paragraphs right column). The short nucleotide sequence selected by Kim contains two hexamer motifs surrounding a spacer region of 8 nucleotides (page 108, Table 1). By replacing this essential part with mutated oligomers (page 107, full right column), Kim demonstrated the importance of the two hexamer sequence elements. Kim thus found that promoters consist of essential elements which can readily be identified with the help of deletion experiments in combination with a standard search for sequence motifs. The symmetric structure of the hexamers identified by Kim is readily visualized by a person skilled in the art. A symmetric structure consisting of a spacer region surrounded by hexamers or palindromes can be identified by pure sequence analysis with or without the help of computer algorithms. Additionally, Kim supports a proposition that mutations in these sequence elements do not necessarily abolish promoter activity. To the contrary, Kim shows that only 20 nucleotides out of 30 identified by deletion analysis are important for promoter activity. Kim also shows that mutations in the 20 nucleotides left, like changing one hexamer of the sequence to a palindrome, does improve promoter activity. Changing the spacer region to a symmetric sequence does improve the promoter activity even further (page 110, Table 3, *nos*, 128-CG and *ocs*). Thus Kim discloses that a 30 base pair element can be narrowed down to 20 nucleotides, of which 10 can be mutated, losing promoter activity only in two constructs. Thus Kim has demonstrated that even in this small element of 30 base pairs, shown to be essential for promoter activity, more than 30% of the bases can be mutated without loosing the activity.

Likewise, Benfey also supports enablement. Benfey describes a detailed analysis of *cis* elements of the 35S promoter of cauliflower mosaic virus (CaMV) by dissecting the 35S promoter into subdomains. The fragments tested in Benfey are short fragments of about 50 bp.

Only fragment B4 has a size of about 100 bp (Fig 1. A at page 960). Even when combined, the tested fragment combinations do not have a fragment size of more than about 200 bp. (e.g., Fragment B5 + B4 plus TATA fragment or the A domain, see Fig 1. A at page 960). Thus, the tested fragments represent much less than what a person skilled in the art would expect to be a minimal promoter showing the same expression pattern. Because of the small fragment size, it is not surprising that those short fragments do not possess the same expression pattern as the original promoter.

Furthermore, Benfey supports the proposition that it is routine to one skilled in the art to obtain a promoter fragment (e.g. a fragment containing nucleotide 300 to nucleotide 583 of SEQ ID NO: 1) with the same expression pattern by a simple deletion analysis. In fact, it was such a deletion analysis that was used initially in Benfey's study of the 35S promoter subdomains. Similar deletion analysis was also used in the study of the regulatory region of the EPSPS gene as discussed in Benfey at page 963, left column, 2nd full paragraph.

Additionally, Benfey shows that a search for known sequence elements and tandem repeats does signify a skilled artisan where sequence mutations are likely affect the function of a promoter and thereby its expression pattern. For instance, by sequence analysis, Benfey identifies two putative CCAAT box sequences and a TGACG tandem repeat in the A domain fragment (page 964). Using site-directed mutagenesis, Benfey shows that the TGACG tandem repeats, but not the CCAAT boxes, are essential elements for the A domain fragment function (page 964, left column, last full paragraph). Thus, consistent with the teaching in Kim, Benfey demonstrates through simple mutagenesis experiments, in combination with a search for known or predicated promoter boxes, that a person of skill in the art could identify which regions or elements of the promoter are essential for preserving function and any mutations in the essential elements would affect activity.

All three references cited by the Examiner show that promoter fragments with a particular activity can be identified by standard deletion experiments, that essential sequence elements can be predicted and identified by sequence analysis, and that those sequence elements represent only a minor part of the promoter sequence. By showing which parts of the promoter sequence are essential through routine experimentation and that only small parts of the original promoter sequence are necessary for activity, Donald, Kim, and Benfey demonstrate that it is

readily within the skill of the art to determine which parts of a promoter sequence can be changed, which substitutions can (or cannot) be made which will affect activity. A skilled artisan would recognize most of a promoter sequence might be changed without losing promoter activity.

Furthermore, identifying regions of a particular promoter sequence that are essential for the specific promoter activity is routine and not undue. As known to one skilled in the art, regions essential for promoter activity often demonstrate clusters of certain, known promoter elements. Such promoter elements can be identified by art-recognized computer algorithms that are specifically developed and adopted for the analysis of plant genes. Once identified, it would be apparent to one skilled in the art which regions of the promoter sequence are likely important to the promoter function and should not be modified in light of the teaching in Kim. Conversely, regions identified as low or no importance for promoter function would be expected to be more tolerant to modification or deletion as shown in Donald. Numerous computer algorithms and databases were made publicly available for such prediction at the time of filing, such as PLACE (Higo et al., Nucleic Acids Research, 1999, 27(1): 297-300, also used in the Examples of the present application), the BIOBASE database "TRANSFAC" (Wingender et al., Nucleic Acids Research, 2001, 29(1): 281-283 and Matys et al., Nucleic Acids Research, 2003, 31(1): 374-378) and the database PlantCARE (Lescot et al., Nucleic Acids Research, 2002, 30(1): 325-327), just to name a few. The applicability of these algorithms and databases in promoter elements prediction can be further evidenced by Steffens et al. (Nucleic Acids Research, 2004, 32: D368-D372), where an Arabidopsis genomic map for transcription regulatory factor binding sites (*i.e.* AthaMap) was created with the aid of the database TRANSFAC and the pattern search program Patser. The creation of AthaMap demonstrates that one skilled in the art would be able to predict the transcription factor binding sites within a sequence of interest using the publicly available databases and pattern search programs and algorithms before carrying out actual experimentation to refine and/or validate the computer predicted sequence information or to modify or delete the promoter sequence while maintaining the promoter activity.

Even further, as discussed in Kolchanov *et al.* (Nucleic Acids Research, 2002, 30(1): 312-317) and Sandelin *et al.* (Nucleic Acids Research, 2004, 32: D9l-D94), the importance of single nucleotides of a transcription factor binding site can be predicted and determined using

these computer programs. Together with the teaching of Kim, one skilled in the art would know to avoid introducing any modification, change, or deletion into those nucleotides in order to preserve the promoter activity. In sum, these references evidence the availability of the various different databases and sequence analysis tools that are specifically designed and adopted to predict the promoter elements at the time of filing. Additionally, these references further demonstrate that a skilled artisan would be able to identify important parts of a promoter sequence using these databases or sequence analysis tools. Once a transcription factor binding site profile of a particular sequence is obtained, one skilled in the art would be able to identify regions of promoter sequence that can be modified or deleted without affecting the promoter function using any conventional method known in the art.

Additionally, the present application describes that the delimitation of the promoter sequence to certain essential regulatory regions can be carried out through routine experimentation (see specification at page 28, line 42 through page 29, line 9). Moreover the specification provides detailed guidance on determining promoter expression and activity, for example at pages 54-57 (Examples 6-8). The specification further provides detailed guidance on cloning the promoters of the invention into a vector as exemplified in Example 3 and on transformation in Example 5. Additionally, the specification also provides detailed guidance on the promoter elements analysis using PLACE algorism (Example 14), as well as guidance on deletion analysis (Example 12) and in vivo mutagenesis (Example 13). In view of the detailed description and guidance provided in the specification as exemplified above, one skilled in the art would recognize that screening and testing for promoter activity is routine and is not undue experimentation. The same applies to screening and testing the promoter activity of fragments of SEQ ID NO: 1 or variants with 98% identity to SEQ ID NO: 1 as claimed in the present application, as evidenced by Donald, Kim, and Benfey cited by the Examiner. It is therefore respectfully submitted that determining the functional activity of individual species of the limited genus being claimed is routine experimentation and not undue experimentation. Compare, *In re Wands*, 858 F.2d 731, 737 (Fed. Cir. 1988) (routine screening of hybridomas was not "undue experimentation;" the involved experimentation can be considerable, so long as "routine"). The test for whether experimentation is "undue" is not merely quantitative, since a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the

experimentation should proceed to enable the determination of how to practice a desired embodiment of the invention claimed. *Ex parte Jackson*, 217 USPQ 804, 807 (1982). In the present case, the specification provides detailed guidance and teaches in the Examples, as explained above, the types of routine assay which are employed to confirm the claimed activity and additionally working examples showing activity. The detailed guidance provided in the present specification and the routine nature of the screening for the claimed activity overcomes the unpredictability alleged by the Examiner.

Thus, from a promoter sequence and a description of its promoter activity, a person of ordinary skill in the art can readily identify related promoter embodiments with promoter activity and the important sequence elements contained therein by using routine experimentation as described in the present application and as demonstrated by Donald, Kim, Benfey, and other additional references cited in this response. Furthermore, the person of skill in the art can readily identify the nucleotides in the promoter sequence which are not essential to the promoter activity and can be changed or deleted without affecting the promoter activity. By using routine experimentation, a person skilled in the art would be readily able to construct promoter fragments and variants that preserve the claimed promoter activity.

In view of the detailed description, guidance, working examples, and high level of skill, the specification enables the full scope of the present claims without undue experimentation. On these facts, an analysis under *In re Wands* supports enablement. For these reasons and in light of the amendment, reconsideration and withdrawal of this rejection is respectfully urged.

The Examiner further cites the thesis by David Phillip Bown (hereinafter "Bown") to support the allegation that the tissue specificity is unpredictable and is species-dependent, and thus, claims to particular tissue specificity are enabled only of the plants in which a tissue-specificity has been determined. Applicants respectfully disagree and strongly urge reconsideration and withdrawal of the rejection for the following reasons.

Bown discloses that the endogenous pPP590 gene (i.e. the ptxA gene) in *Pisum Sativum* expresses strongly in pods, but not in leaves, and weakly or not expressed in petals (page 126). As the Examiner correctly noted, this data refers only to the endogenous expression of the ptxA gene, but not the **isolated ptxA promoter** as claimed. It is known in the art that the activity of an isolated promoter is not always identical with the expression level of a naturally occurring

endogenous gene in a particular tissue. Two possible reasons may affect the expression pattern of an endogenous gene. First, the expression activity of an endogenous gene may be influenced by its genomic environment of the locus. For instance, Zubko *et al.* suggests that tissue specific silencing plays a role in adjusting the expression pattern of the *Sho* gene from *Petunia hybrida* (see Summary at page 1131, Plant Journal, 2007, 52: 1131-1139, copy enclosed). Second, the mRNA level in particular tissues may be influenced by additional control mechanism such as RNA silencing *via* miRNAs (see e.g., Wang et al., Frontiers in Bioscience, 2007, 12: 3975-3982). Both mechanisms are specific to the coding sequence and independent of the promoter sequence. Accordingly, what observed by Bown is the expression pattern of the ptxA gene in its natural genomic environment, taking into account of all potential control mechanisms. Conversely, the expression pattern of the **isolated ptxA promoter** is shown to have similar expression pattern in Arabidopsis and Canola in the present application (see Example 7 at pages 55-56).

Similarly, what is observed with the tomato TPRP-F1 gene (discussed in Bown, page 158) is the expression pattern detected in its natural genomic environment, not the expression pattern of the **isolated** promoter. Furthermore, although the tomato TPRP-F1 gene shares 88% identity at the amino acid level and 79% identity at the nucleic acid level with the pPP590 gene, nothing indicates that this is actually the corresponding pPP590 gene in tomato (see page 158). Additionally, a sequence alignment fails to show any significant sequence identity between the ptxA promoter and the TPRP-F1 promoter (GenBank Accession X61395).

It is noted that the Examiner has taken an inconsistent position in making this rejection based on Bown. On one hand, the Examiner alleges that the tissue-specificity of the ptxA promoter is highly unpredictable. Office Action at page 16, line 20. On the other hand, the Examiner states that "one would predict that the ptxA promoter might drive expression predominantly in young tomato fruit if transformed into a tomato plant" in view of the expression pattern of the tomato homolog. Office Action at page 16, lines 18-20 (emphasis added). Nevertheless, based on the teaching of the art that the expression pattern of an endogenous gene in its natural genomic environment depends not only on it regulatory promoter, but also other control mechanisms, the observation of Bown cannot be a comparable basis to conclude that an **isolated** ptxA promoter would have a different expression pattern in tomato or

any species other than Arabidopsis or Canola. Additionally, the present application does show a consistent expression pattern in two species. Reconsideration and withdrawal of this rejection is respectfully requested.

The Examiner further rejects claim 13 for lack of enablement arguing that one skilled in the art would not know how to use a yeast, algae or fungi transformed with a construct comprising the ptxA promoter because this promoter is allegedly unlikely to be active in those organisms. Applicants disagree.

It is noted that claim 13 also recites bacteria, which are not included in this rejection. Thus, a fair reading of the rejection indicates that the Examiner acknowledges the utility of bacteria as a transgenic organism containing the claimed construct. It is well recognized in the art that, not only bacteria, but also yeast, algae, or fungi can be used to multiply or maintain an expression construct such as the one encompassed by claim 1. Claim 13 does not require that the expression construct be expressed in the transgenic organism containing the same. A perfect example is the bacterial host cell containing the expression construct for cloning purposes as acknowledged by the Examiner. Thus, whether the promoter will be active in the host organism is irrelevant to what is claimed in claim 13. Reconsideration and withdrawal of the rejection is respectfully requested.

Rejections under 35 U.S.C. § 102(b)

Claims 1, 3, 7-15, and 22-24 are rejected as being anticipated under U.S.C. § 102(b) by Donald et al. (hereinafter "Donald"). The Examiner alleges that the promoter taught in Donald is inherently able to hybridize to a fragment of at least 50 nucleotides of SEQ ID NO: 1 under some stringency conditions. Applicants respectfully disagree. However, to expedite the prosecution, the claims have been amended without prejudice or disclaimer to recite the components of the claimed expression cassette with more specificity. It is believed that the present amendment renders the rejection moot.

Claims 15 and 24 are rejected under 35 USC §102(b) as being anticipated by Khan. In light of the present amendment, it is believed that the rejection is moot.

Rejections under 35 U.S.C. § 103(a)

Claims 1, 3, 8-15 and 22-25 are rejected under 35 USC §103(a) as being obvious over Henkes et al. (hereinafter "Henkes") in view of Bown (GenBank Accession No. X67427, hereinafter "Bown-2"). Claims 1, 3, 8-15 and 22-25 are further rejected under 35 USC §103(a) as being obvious over Arntzen et al. (hereinafter "Arntzen") in view of Bown-2 and Bown. Applicants respectfully disagree and traverse both the rejections for the following reasons.

To support a *prima facie* conclusion of obviousness, the prior art must disclose or suggest all the limitations of the claimed invention. See *In re Lowry*, 32 F.3d 1579, 1582 (Fed. Cir. 1994).

The Examiner relies on Henkes for teaching a construct comprising a "super promoter," and identifying the ptxA promoter as a stress inducible promoter that is useful for the construct taught therein. The Examiner acknowledges that Henkes does not teach the sequence of SEQ ID NO: 1, but relies on Bown for such teaching. The Examiner also acknowledges that Henkes does not teach any tissue specificity of expression, but argues that the tissue specificity as recited in claim 1 is an intrinsic property of the ptxA promoter. Applicants respectfully disagree.

As depicted in Figure 1, the construct taught in Henkes comprises a "super promoter" and a "desired gene." Henkes defines the "desired gene" as an AOXSRP coding nucleic acid (paragraph [0029]), the expression of which in the plant results in increased tolerance to environmental stress. See Abstract. Henkes does not teach, or even suggest, that the "desired gene" could be a selection marker, a reporter gene, or a nucleic acid sequence which, when expressed, results in the production of an antisense RNA or double-stranded RNA, or increases quality of food and feed, produces chemicals, fine chemicals or pharmaceuticals, or confers resistance to herbicides or male sterility. Even taken in view of Bown-2, Henkes does not teach or suggest an expression construct as now claimed.

Furthermore, it is respectfully submitted that a person skilled in the art would not have had the motivation to combine a stress inducible promoter (*i.e.* the ptxA promoter as characterized in Henkes and Bown) with any of the nucleic acid sequences recited in claim 1 because those genes are related to traits that are stress-independent. Additionally, one of ordinary skill in the art would not have had a reasonable expectation of success that the ptxA promoter would drive the expression of any of those genes in a vegetative-tissue specific fashion

in view of the teaching in Henkes. Thus, Henkes, alone or in combination with Bown, does not teach or suggest the expression construct as claimed.

Claims 1, 3, 8-15 and 22-25 are further rejected under 35 USC §103(a) as being obvious over Arntzen (hereinafter "Arntzen") in view of Bown and Bown-2. The Examiner relies on Arntzen for teaching transgenic plants expressing oral (edible) antigen in plant tissues and vectors comprising an expression cassette. The Examiner acknowledges that Arntzen does not teach the ptxA promoter, expression in vegetative tissues but not in seeds, or expression of GUS, but relied on Bown and Bown-2 for such teaching. Specifically, the Examiner argues that the ptxA promoter mediates expression in editable portions of a plant because Bown teaches the expression of an endogenous gene that is naturally connected to this promoter in pea seed pods and in young tomato fruits. Additionally, the Examiner also alleges that the tissue specificity is an intrinsic property of the ptxA promoter that would naturally flow from the combination of Arntzen, Bown, and Bown-2. Applicants respectfully disagree.

Arntzen teaches transgenic production of oral antigens in the edible plant materials. Arntzen defines an edible plant material to include a plant or any material obtained from a plant which is suitable for ingestion by mammal or other animals including humans (Col. 12, lines 11-13). Thus, edible plant parts, by default, will include almost all of the plant parts such as plant parts having only vegetative tissues (e.g. leaves and stems), plant parts having vegetative tissues and generative tissues (e.g. tomato fruits and pea seed pods), or plant parts having only generative tissues (e.g. seeds).

As discussed in the enablement section above, Bown teaches predominant expression in seed pots and weak (or no) expression in petals of pea, and explicitly states that **no expression was observed in leaves** (page 126, second paragraph). This result strongly suggests a **seed pot specific** expression pattern, but not other edible parts of a plant such as leaves (i.e. vegetative tissue). Thus, even when combined, Arntzen and Bown teach an expression pattern that is limited to edible plant parts having only generative tissues such as seed pots. As explicitly taught in Bown, the transgenic plants obtained from such combined teaching would **NOT** have an intrinsic property to express in the vegetative tissues such as leaves as alleged by the Examiner.

Similarly, the expression pattern of the tomato homolog discussed in Bown does not remedy this deficiency. The tomato homolog was highly expressed in young tomato fruits but very low (or no expression) in stem, root, etiolated seedlings, leaf and mature-green and ripe fruits. Such expression pattern indicates the specificity in young fruits but not in edible plant parts. Thus, one skilled in the art would not have been motivated by such teaching to use the promoter from the tomato homolog to express an antigen in the edible plant materials. Even if such transgenic plant is so produced, the transgene would not have been intrinsically expressed in the edible plant materials such as vegetative tissues as alleged by the Examiner.

For the above reasons, it is submitted that Arntzen, Bown, and Bown-2, alone or in combination, would not have rendered the present application obvious. Reconsideration and withdrawal of the rejection is respectfully requested.

CONCLUSION

For at least the above reasons, Applicants respectfully request withdrawal of the rejections and allowance of the claims.

Applicants reserve all rights to pursue the non-elected claims and subject matter in one or more divisional applications.

Accompanying this response is a petition for a one-month extension of time to and including July 13, 2008 to respond to the Office Action mailed March 13, 2008 with the required fee authorization. No further fee is believed due. However, if any fee is due, the Director is hereby authorized to charge our Deposit Account No. 03-2775, under Order No. 13987-00021-US from which the undersigned is authorized to draw.

Respectfully submitted,

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Attachment: Zubko *et al.*, A natural antisense transcript of the *Petunia hybrida Sho* gene suggests a role for an antisense mechanism in cytokinin regulation. Plant Journal, 2007, 52: 1131-1139.